

SEQUENCE LISTING

<110> Curiel, David T.  
Krasnykh, Victor N.

<120> Modified Adenovirus Containing A Fiber  
Replacement Protein

<130> D6070CIP

<141> 2000-07-10

<150> US 09/250,580  
US 60/074,844

<151> 1999-02-16  
1998-02-17

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<212> DNA

<213> artificial sequence

<220>

<221> primer\_bind

<223> Forward primer FF.F used to amplify segment of the T4  
fibritin gene encoding amino acids Ser-229 through  
the carboxy terminal Ala-487.

<400> 1

gggaacttga cctcacagaa cgtttatagt cgtttaaatg 40

<210> 2

<211> 37

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<220>

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<223> Reverse primer FF.R used to amplify segment of the T4  
fibritin gene encoding amino acids Ser-229 through  
the carboxy terminal Ala-487.

<400> 2

aggccatggc caattttgc cggcgataaa aaggtag 37

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<223> synthetic oligo, F5. $\Delta$ 3Swa.T, for the introduction of  
SwaI restriction site  
<400> 3

ttggcccat ttaaatgaat cgtttgtt atgttcaac gtgttattt ttc 53

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SwaI restriction site  
<400> 4

aattgaaaaa taaaacacgtt gaaacataac acaaacgatt cattaaatg 50  
ggccaatat t 61

<210> 5  
<211> 57  
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<223> synthetic oligo, FF<sub>BB</sub>LL.T  
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ggcaggtgga ggcgttcag gcggaggtgg ctctggcggt ggcggatccg 50  
gggattt 57

<210> 6

<211> 57  
<212> DNA  
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<400> 6

aaatccccgg atccgccacc gccagagcca cctccgcctg aaccgcctcc 50  
acctgcc 57

<210> 7  
<211> 36  
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<400> 7

gatctagagg atcgcacac catcaccatc actaat 36

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attagtgtat gtgatggta tgcgatcctc ta 32

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<221> primer\_bind  
<223> primer to PCR amplify FF/6H in pXK.FF/6H

<400> 9

ccctcatgaa gcgcgcaaga ccgtctg 27

<210> 10

<211> 27

<212> DNA

<213> artificial sequence

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<221> primer\_bind

<223> primer to PCR amplify FF/6H in pXK.FF/6H

<400> 10

cccaagctta gtgatggta tggat 27

<210> 11

<211> 8

<212> PRT

<213> Adenovirus type 5

<220>

<221> DOMAIN

<223> the beginning of the third pseudorepeat of the  
fiber shaft domain

<400> 11

Gly Asn Thr Leu Ser Gln Asn Val

5 8

<210> 12

<211> 26

<212> PRT

<213> Phage T4

<220>

<221> DOMAIN

<223> the sixth coiled coil segment of the  $\alpha$ -helical  
central domain of the fibritin

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Val Tyr Ser Arg Leu Asn Glu Ile Asp Thr Lys Gln Thr Thr Val

5 10

15

Glu Ser Asp Ile Ser Ala Ile Lys Thr Ser Ile

20

25

<210> 13  
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<212> PRT  
<213> artificial sequence  
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<221> CHAIN  
<223> the fiber-fibritin-6H chimera  
<400> 13

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr  
5 10 15  
Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr  
20 25 30  
Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly  
35 40 45  
Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly  
50 55 60  
Met Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly  
65 70 75  
Asn Leu Thr Ser Gln Asn Val Tyr Ser Arg Leu Asn Glu Ile Asp  
80 85 90  
Thr Lys Gln Thr Thr Val Glu Ser Asp Ile Ser Ala Ile Lys Thr  
95 100 105  
Ser Ile Gly Tyr Pro Gly Asn Asn Ser Ile Ile Thr Ser Val Asn  
110 115 120  
Thr Asn Thr Asp Asn Ile Ala Ser Ile Asn Leu Glu Leu Asn Gln  
125 130 135  
Ser Gly Gly Ile Lys Gln Arg Leu Thr Val Ile Glu Thr Ser Ile  
140 145 150  
Gly Ser Asp Asp Ile Pro Ser Ser Ile Lys Gly Gln Ile Lys Asp  
155 160 165  
Asn Thr Thr Ser Ile Glu Ser Leu Asn Gly Ile Val Gly Glu Asn  
170 175 180  
Thr Ser Ser Gly Leu Arg Ala Asn Val Ser Trp Leu Asn Gln Ile

185                    190                    195  
Val Gly Thr Asp Ser Ser Gly Gly Gln Pro Ser Pro Pro Gly Ser  
                      200                    205                    210  
Leu Leu Asn Arg Val Ser Thr Ile Glu Thr Ser Val Ser Gly Leu  
                      215                    220                    225  
Asn Asn Asp Val Gln Asn Leu Gln Val Glu Ile Gly Asn Asn Ser  
                      230                    235                    240  
Thr Gly Ile Lys Gly Gln Val Val Ala Leu Asn Thr Leu Val Asn  
                      245                    250                    255  
Gly Thr Asn Pro Asn Gly Ser Thr Val Glu Glu Arg Gly Leu Thr  
                      260                    265                    270  
Asn Ser Ile Lys Ala Asn Glu Thr Asn Ile Ala Ser Val Thr Gln  
                      275                    280                    285  
Glu Val Asn Thr Ala Lys Gly Asn Ile Ser Ser Leu Gln Gly Asp  
                      290                    295                    300  
Val Gln Ala Leu Gln Glu Ala Gly Tyr Ile Pro Glu Ala Pro Arg  
                      305                    310                    315  
Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu  
                      320                    325                    330  
Ser Thr Phe Leu Ser Pro Ala Gly Gly Gly Ser Gly Gly Gly  
                      335                    340                    345  
Gly Ser Gly Gly Gly Ser Arg Gly Ser His His His His His  
                      350                    355                    360  
His  
361

<210>      14  
<211>      9  
<212>      PRT  
<213>      Unknown  
<220>  
<221>      DOMAIN  
<223>      a peptide ligand containing the RGD motif  
<400>      14

Cys Asp Cys Arg Gly Asp Cys Phe Cys